

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/536,586
Source: PCT
Date Processed by STIC: 05/18/2006

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 05/18/2006

PATENT APPLICATION: US/10/536,586

TIME: 10:09:27

Input Set : A:\082368-004500US.txt

Output Set: N:\CRF4\05182006\J536586.raw

4 <110> APPLICANT: Takeuchi, Masakazu
 5 Sato, Keiko
 6 Sakamoto, Yoshimasa
 7 Tawarada, Maki
 8 Ohtsuka, Toshihisa
 10 <120> TITLE OF INVENTION: MAMMALIAN PRICKLE GENE
 12 <130> FILE REFERENCE: 082368-004500US
 14 <140> CURRENT APPLICATION NUMBER: 10/536,586
 C--> 15 <141> CURRENT FILING DATE: 2005-05-26
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/015223
 18 <151> PRIOR FILING DATE: 2003-11-28
 20 <150> PRIOR APPLICATION NUMBER: JP 2002-346447
 21 <151> PRIOR FILING DATE: 2002-11-28
 23 <160> NUMBER OF SEQ ID NOS: 3
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 847
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Rattus norvegicus
 32 <400> SEQUENCE: 1
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 34 1 5 10 15
 35 Met Phe Asp Phe Gln Arg Asn Ser Thr Ser Asp Asp Asp Ser Gly Cys
 36 20 25 30
 37 Ala Leu Glu Glu Tyr Ala Trp Val Pro Pro Gly Leu Lys Pro Glu Gln
 38 35 40 45
 39 Val His Gln Tyr Tyr Ser Cys Leu Pro Glu Glu Lys Val Pro Tyr Val
 40 50 55 60
 41 Asn Ser Pro Gly Glu Lys Leu Arg Ile Lys Gln Leu Leu His Gln Leu
 42 65 70 75 80
 43 Pro Pro His Asp Asn Glu Val Arg Tyr Cys Asn Ser Leu Asp Glu Glu
 44 85 90 95
 45 Glu Lys Arg Glu Leu Lys Leu Phe Ser Asn Gln Arg Lys Arg Glu Asn
 46 100 105 110
 47 Leu Gly Arg Gly Asn Val Arg Pro Phe Pro Val Thr Met Thr Gly Ala
 48 115 120 125
 49 Ile Cys Glu Gln Cys Gly Gly Gln Ile Lys Gly Gly Asp Ile Ala Val
 50 130 135 140
 51 Phe Ala Ser Arg Ala Gly His Gly Ile Cys Trp His Pro Pro Cys Phe
 52 145 150 155 160
 53 Ile Cys Thr Val Cys Asn Glu Leu Leu Val Asp Leu Ile Tyr Phe Tyr
 54 165 170 175
 55 Gln Asp Gly Lys Ile Tyr Cys Gly Arg His His Ala Glu Cys Leu Lys

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56          180          185          190
57 Pro Arg Cys Ala Ala Cys Asp Glu Ile Ile Phe Ala Asp Glu Cys Thr
58          195          200          205
59 Glu Ala Glu Gly Arg His Trp His Met Arg His Phe Cys Cys Phe Glu
60          210          215          220
61 Cys Glu Thr Val Leu Gly Gly Gln Arg Tyr Ile Met Lys Glu Gly Arg
62 225          230          235          240
63 Pro Tyr Cys Cys His Cys Phe Glu Ser Leu Tyr Ala Glu Tyr Cys Asp
64          245          250          255
65 Thr Cys Ala Gln His Ile Gly Ile Asp Gln Gly Gln Met Thr Tyr Asp
66          260          265          270
67 Gly Gln His Trp His Ala Thr Glu Asn Cys Phe Cys Cys Ala His Cys
68          275          280          285
69 Lys Lys Ser Leu Leu Gly Arg Pro Phe Leu Pro Lys Gln Gly Gln Ile
70          290          295          300
71 Phe Cys Ser Arg Ala Cys Ser Ala Gly Glu Asp Pro Asn Gly Ser Asp
72 305          310          315          320
73 Ser Ser Asp Ser Ala Phe Gln Asn Ala Arg Ala Lys Glu Ser Arg Arg
74          325          330          335
75 Ser Ala Lys Ile Gly Lys Asn Lys Gly Lys Thr Glu Glu Thr Met Leu
76          340          345          350
77 Asn Gln His Ser Gln Leu Gln Val Ser Ser Asn Arg Leu Ser Ala Asp
78          355          360          365
79 Val Asp Pro Leu Ser Val Gln Met Asp Leu Leu Ser Leu Ser Ser Gln
80          370          375          380
81 Thr Pro Ser Leu Asn Arg Asp Pro Ile Trp Arg Ser Arg Asp Glu Pro
82 385          390          395          400
83 Phe His Tyr Gly Asn Lys Met Glu Gln Asn Gln Ser Gln Ser Pro Leu
84          405          410          415
85 Gln Leu Leu Ser Gln Cys Asn Ile Arg Thr Ser Tyr Ser Pro Gly Gly
86          420          425          430
87 Gln Ala Ala Gly Ala Gln Pro Asp Met Trp Ala Lys His Phe Ser Asn
88          435          440          445
89 Pro Lys Arg Ser Ser Ser Met Ala Leu Lys Gly His Gly Gly Ser Phe
90          450          455          460
91 Ile Gln Glu Cys Arg Glu Asp Tyr Tyr Pro Gly Arg Leu Met Ser Gln
92 465          470          475          480
93 Glu Ser Tyr Ser Asp Met Ser Ser Gln Ser Phe Ser Glu Thr Arg Gly
94          485          490          495
95 Ser Ile Pro Val Pro Lys Tyr Glu Glu Glu Glu Glu Glu Glu Glu
96          500          505          510
97 Glu Gly Gly Ile Ser Thr Gln Gln Cys Arg Pro Arg Arg Pro Leu Ser
98          515          520          525
99 Ser Leu Lys Tyr Thr Glu Asp Met Thr Pro Thr Glu Gln Thr Pro Arg
100          530          535          540
101 Gly Ser Met Glu Ser Leu Ala Leu Ser Asn Ala Thr Gly Leu Ser Ala
102 545          550          555          560
103 Glu Gly Gly Ala Lys Arg Gln Glu His Leu Ser Arg Phe Ser Met Pro
104          565          570          575

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105 Asp Leu Ser Lys Asp Ser Gly Met Asn Val Ser Glu Lys Leu Ser Asn
106          580          585          590
107 Met Gly Thr Leu Asn Ser Ser Met Gln Phe Arg Ser Ala Glu Ser Val
108          595          600          605
109 Arg Ser Leu Leu Ser Ala Gln Tyr Gln Glu Met Glu Gly Asn Leu
110          610          615          620
111 His Gln Leu Ser Asn Pro Leu Gly Tyr Arg Asp Leu Gln Ser His Gly
112 625          630          635          640
113 Arg Met His Gln Ser Phe Asp Phe Asp Gly Gly Ile Ala Ser Ser Lys
114          645          650          655
115 Leu Pro Gly Gln Glu Gly Val His Ile Gln Pro Met Ser Glu Arg Thr
116          660          665          670
117 Arg Arg Arg Thr Thr Ser Arg Asp Asp Asn Arg Arg Phe Arg Pro His
118          675          680          685
119 Arg Ser Arg Arg Ser Arg Arg Ser Arg Ser Asp Asn Ala Leu His Leu
120          690          695          700
121 Ala Ser Glu Arg Glu Val Ile Ala Arg Leu Lys Asp Arg Pro Pro Leu
122 705          710          715          720
124 Arg Ala Arg Glu Asp Tyr Asp Gln Phe Val Arg Gln Arg Ser Phe Gln
125          725          730          735
126 Glu Ser Met Gly Gln Gly Ser Arg Arg Asp Leu Tyr Ser Gln Cys Pro
127          740          745          750
128 Arg Thr Val Ser Asp Leu Ala Leu Gln Asn Ala Phe Gly Glu Arg Trp
129          755          760          765
130 Gly Pro Tyr Phe Thr Glu Tyr Asp Trp Cys Ser Thr Cys Ser Ser Ser
131          770          775          780
132 Ser Glu Ser Asp Asn Glu Gly Tyr Phe Leu Gly Glu Pro Ile Pro Gln
133 785          790          795          800
134 Pro Ala Arg Leu Arg Tyr Val Thr Ser Asp Glu Leu Leu His Lys Tyr
135          805          810          815
136 Ser Ser Tyr Gly Val Pro Lys Ser Ser Thr Leu Gly Gly Arg Gly Gln
137          820          825          830
138 Leu His Ser Arg Lys Arg Gln Lys Ser Lys Asn Cys Ile Ile Ser
139          835          840          845
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 3385
144 <212> TYPE: DNA
145 <213> ORGANISM: Rattus norvegicus
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (403)...(2943)
151 <400> SEQUENCE: 2
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153 aggcctagaa caagggcaca agtcgcactc tctggcttgg tggatctcta gcagggctctg 120
154 ctttcagggga gggcgttctc tcggagggaa tgcaaaagaa gaccggtttg ggtttgagcc 180
155 tgctgcctgc ctccggaagg gctcagattc gcagagactc tgtaaaggag atgtttgggc 240
156 tgcctggggt cctgcttgca ttttctggta ccagctccag ggggaaagtg aactggggca 300
157 actgaccaga tcaagactcg gtggcggtt cttctaaagc ttcgcggctc atcctctagg 360
158 aggaagatct gcctgcactg caagtgtccc caggaggagc ac atg gtg aca gtg 414

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159														Met	Val	Thr	Val	
160														1				
162	atg	ccg	ctg	gag	atg	gag	aag	acc	att	agc	aag	ctc	atg	ttt	gac	ttc		462
163	Met	Pro	Leu	Glu	Met	Glu	Lys	Thr	Ile	Ser	Lys	Leu	Met	Phe	Asp	Phe		
164	5					10					15					20		
166	cag	agg	aat	tca	acc	tca	gat	gac	gac	tcg	ggc	tgt	gct	ttg	gaa	gaa		510
167	Gln	Arg	Asn	Ser	Thr	Ser	Asp	Asp	Asp	Ser	Gly	Cys	Ala	Leu	Glu	Glu		
168					25					30					35			
170	tat	gcc	tgg	gtc	ccc	ccg	ggg	ctg	aag	cct	gag	cag	gtg	cac	cag	tat		558
171	Tyr	Ala	Trp	Val	Pro	Pro	Gly	Leu	Lys	Pro	Glu	Gln	Val	His	Gln	Tyr		
172				40					45					50				
174	tat	agc	tgc	ctc	cca	gaa	gag	aaa	gtt	ccc	tat	gtc	aac	agc	cct	gga		606
175	Tyr	Ser	Cys	Leu	Pro	Glu	Glu	Lys	Val	Pro	Tyr	Val	Asn	Ser	Pro	Gly		
176			55					60					65					
178	gag	aaa	ttg	cga	atc	aag	cag	cta	ctg	cac	cag	ctg	cca	ccc	cac	gac		654
179	Glu	Lys	Leu	Arg	Ile	Lys	Gln	Leu	Leu	His	Gln	Leu	Pro	Pro	His	Asp		
180		70				75					80							
182	aat	gag	gtt	cgg	tat	tgc	aac	tcc	ctg	gac	gag	gag	gag	aag	cgg	gag		702
183	Asn	Glu	Val	Arg	Tyr	Cys	Asn	Ser	Leu	Asp	Glu	Glu	Glu	Lys	Arg	Glu		
184	85					90					95					100		
186	ctg	aag	ctg	ttc	agc	aac	cag	agg	aaa	cgt	gag	aac	ctg	ggc	cga	ggc		750
187	Leu	Lys	Leu	Phe	Ser	Asn	Gln	Arg	Lys	Arg	Glu	Asn	Leu	Gly	Arg	Gly		
188				105						110					115			
190	aat	gtc	agg	ccc	ttc	ccc	gtc	acc	atg	aca	ggg	gct	att	tgc	gaa	cag		798
191	Asn	Val	Arg	Pro	Phe	Pro	Val	Thr	Met	Thr	Gly	Ala	Ile	Cys	Glu	Gln		
192				120						125				130				
194	tgt	gga	ggt	cag	att	aag	ggc	ggc	gac	atc	gct	gtg	ttt	gca	tca	cgt		846
195	Cys	Gly	Gly	Gln	Ile	Lys	Gly	Gly	Asp	Ile	Ala	Val	Phe	Ala	Ser	Arg		
196			135					140					145					
198	gct	ggc	cat	ggc	atc	tgc	tgg	cat	cca	cca	tgc	ttt	ata	tgc	aca	gtc		894
199	Ala	Gly	His	Gly	Ile	Cys	Trp	His	Pro	Pro	Cys	Phe	Ile	Cys	Thr	Val		
200		150					155					160						
202	tgc	aat	gag	ctt	ctg	gtt	gac	ctg	atc	tac	ttt	tac	caa	gat	ggg	aag		942
203	Cys	Asn	Glu	Leu	Leu	Val	Asp	Leu	Ile	Tyr	Phe	Tyr	Gln	Asp	Gly	Lys		
204	165					170					175					180		
206	atc	tac	tgt	ggc	agg	cac	cat	gct	gag	tgc	ctg	aag	ccg	cgc	tgt	gca		990
207	Ile																	

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224	245				250				255				260				
226	cat	ata	gga	att	gac	caa	ggt	caa	atg	acc	tat	gac	ggc	caa	cac	tgg	1230
227	His	Ile	Gly	Ile	Asp	Gln	Gly	Gln	Met	Thr	Tyr	Asp	Gly	Gln	His	Trp	
228					265				270					275			
230	cat	gct	acg	gag	aac	tgt	ttc	tgc	tgt	gct	cat	tgt	aag	aag	tct	ctc	1278
231	His	Ala	Thr	Glu	Asn	Cys	Phe	Cys	Cys	Ala	His	Cys	Lys	Lys	Ser	Leu	
232					280				285					290			
234	ctg	ggg	cgg	cca	ttc	ctc	ccg	aag	caa	ggc	cag	ata	ttc	tgc	tca	cgg	1326
235	Leu	Gly	Arg	Pro	Phe	Leu	Pro	Lys	Gln	Gly	Gln	Ile	Phe	Cys	Ser	Arg	
236					295				300					305			
238	gcc	tgt	agt	gct	ggg	gag	gac	ccc	aat	ggc	tct	gac	tca	tct	gat	tca	1374
239	Ala	Cys	Ser	Ala	Gly	Glu	Asp	Pro	Asn	Gly	Ser	Asp	Ser	Ser	Asp	Ser	
240					310				315					320			
242	gcc	ttc	cag	aat	gcc	aga	gcc	aag	gag	tct	cgc	cgc	agt	gcc	aaa	att	1422
243	Ala	Phe	Gln	Asn	Ala	Arg	Ala	Lys	Glu	Ser	Arg	Arg	Ser	Ala	Lys	Ile	
244	325					330					335					340	
246	ggc	aag	aac	aag	ggc	aaa	aca	gag	gaa	acc	atg	ctg	aac	cag	cac	agc	1470
247	Gly	Lys	Asn	Lys	Gly	Lys	Thr	Glu	Glu	Thr	Met	Leu	Asn	Gln	His	Ser	
248					345					350					355		
250	cag	ctg	cag	gtg	agt	tct	aac	cgg	ctc	tca	gct	gat	gtg	gac	ccc	ctg	1518
251	Gln	Leu	Gln	Val	Ser	Ser	Asn	Arg	Leu	Ser	Ala	Asp	Val	Asp	Pro	Leu	
252					360				365					370			
254	tca	gtg	cag	atg	gat	ctc	ctc	agc	ctg	tcc	agc	cag	acg	ccc	agc	ctc	1566
255	Ser	Val	Gln	Met	Asp	Leu	Leu	Ser	Leu	Ser	Ser	Gln	Thr	Pro	Ser	Leu	
256					375				380					385			
258	aac	cgg	gac	ccc	att	tgg	agg	agc	cgg	gat	gag	ccc	ttc	cat	tac	ggg	1614
259	Asn	Arg	Asp	Pro	Ile	Trp	Arg	Ser	Arg	Asp	Glu	Pro	Phe	His	Tyr	Gly	
260					390				395				400				
262	aac	aag	atg	gag	cag	aac	caa	tcc	cag	agt	cct	ttg	cag	ctc	ctc	agc	1662
263	Asn	Lys	Met	Glu	Gln	Asn	Gln	Ser	Gln	Ser	Pro	Leu	Gln	Leu	Leu	Ser	
264	405					410					415					420	
266	cag	tgc	aac	atc	aga	acg	tcc	tac	agt	cca	gga	ggg	cag	gca	gca	gga	1710
267	Gln	Cys	Asn	Ile	Arg	Thr	Ser	Tyr	Ser	Pro	Gly	Gly	Gln	Ala	Ala	Gly	
268					425					430					435		
270	gcc	cag	cct	gac	atg	tgg	gcc	aag	cac	ttc	agc	aac	ccc	aag	aga	agc	1758
271	Ala	Gln	Pro	Asp	Met	Trp	Ala	Lys	His	Phe	Ser	Asn	Pro	Lys	Arg	Ser	
272					440				445					450			
274	tca	tca	atg	gcc	ctg	aag	ggg	cac	ggt	ggc	agt	ttt	atc	cag	gaa	tgt	1806
275	Ser	Ser	Met	Ala	Leu	Lys	Gly	His	Gly	Gly	Ser	Phe	Ile	Gln	Glu	Cys	
276					455				460					465			
278	cgt	gag	gac	tat	tac	cca	ggg	agg	ctg	atg	tcc	cag	gag	agc	tac	agc	1854
279	Arg	Glu	Asp	Tyr	Tyr	Pro	Gly	Arg	Leu	Met	Ser	Gln	Glu	Ser	Tyr	Ser	
280					470				475					480			
282	gat	atg	tct	agc	caa	agc	ttt	agt	gaa	acc	cga	ggc	agc	atc	ccg	gtt	1902
283	Asp	Met	Ser	Ser	Gln	Ser	Phe	Ser	Glu	Thr	Arg	Gly	Ser	Ile	Pro	Val	
284	485					490					495					500	
286	ccc	aag	tat	gag	gag	gag	gag	gag	gag	gag	gag	gaa	gaa	ggg	ggc	ata	1950
287	Pro	Lys	Tyr	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Gly	Ile	
288					505				510						515		

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date